9



SEQUENCE LISTING

<110> Allen, Keith D. Zhang, Qin

<120> TRANSGENIC MICE CONTAINING CX2 GENE DISRUPTIONS

<130> R-716

<140> US 09/900,518

<141> 2001-07-06

<150> US 60/216,178

<151> 2000-07-06

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2490

<212> DNA

<213> Mus musculus

TIPE

<400> 1

aggetgtece acceaceate tgeaceeget geagegeeeg egeceetgte eegegeegta 60 gtcgtcattt gtagcccgcc tgccgctccc ggggacccga tcctaccctg ggtgcggggc 120 agagegggea tggeeegtet ggggaeegee tgeeetgege tggegetgge eetggeaett 180 gtggcggtgg ccctggctgg agtcagagcc cagggcgcag ccttcgagga gcctgactat 240 tacagecagg agetetggeg gegegggege tattatggge ateeggagee tgageeggag 300 ccggagctct tctcgccttc aatgcatgaa gaccttaggg tggaggagca ggaacagcag 360 gagccgcacc agcagggcca cagaactccc aagaaggcca tcaagcccaa gaaggctccc 420 aagagggaga agttagttgc agagacgcct ccaccaggta aaaatagcaa cagaaaaggc 480 agaagaagca agaatcttga gaaagctgcc agtgatgacc atggtgtccc tgtggctcat 540 gaggatgtca gagagagttg cccacctctt ggtctggaaa cattaaaaat cacagacttc 600 cagctgcatg cctccacatc gaagcgttat ggcctgggag cccaccgggg gagactcaac 660 atccaggcag gcattaatga aaatgacttt tacgatgggg cttggtgtgc tggtaggaac 720 gacttgcatc agtggatcga agtggatgcc cggcgcctga ccaagttcac aggggtcatt 780 acceaaggaa ggaactetet etggetgagt gaetgggtga cateetataa agteatggtg 840 agcaatgaca gccacacatg ggttactgtg aagaatggat ctggcgacat gatatttgaa 900 ggaaacagtg agaaggagat teetgtgete aatgagetge eagteeecat ggtggeeege 960 tacattcgca taaaccctca gtcctggttt gataacggga gcatctgcat gaggatggag 1020 atcttgggct gcccactgcc ggatcctaat aactattatc accgacgtaa tgagatgacc 1080 accacggatg acctggattt taagcaccac aactataagg aaatgcgcca gttgatgaag 1140 gttgtcaatg aaatgtgccc caatattacc aggatttaca acattggcaa aagccaccag 1200 ggcctgaaat tgtatgcggt agagatetet gaccatectg gggaacatga agttggtgag 1260 cccgagttcc actacatcgc aggggcccac ggcaatgagg ttctgggacg agaactgctg 1320 ctgctgctgc tgcacttcct ctgccaggaa tactcggcgc agaacgcacg catcgtccgc 1380 ttggtggagg agactcgaat ccacattcta ccctccctca atcctgatgg ctatgagaag 1440 gcctatgaag gaggttccga gttgggaggc tggtccctgg gacgttggac ccatgatggc 1500 atcgatatca acaacaactt tccggattta aactcgctgc tctgggaggc agaggaccag 1560 cagaatgccc caaggaaggt ccccaaccac tacattgcca tccctgagtg gtttctgtct 1620 gagaatgcca cagtggccac agagaccaga gccgtcatcg cctggatgga gaagatcccg 1680 tttgtgctgg gaggcaacct acaggggggt gagctggtcg tggcataccc ctatgacatg 1740 gtgcggtccc tgtggaagac ccaggagcac accccaacac ctgatgatca tgtgttccgc 1800 tggctggcgt attectacge etceacteae egeetcatga cagatgecag gaggegagtg 1860 tgccacacgg aagattttca gaaggaggag ggcaccgtca atggggcttc ctggcacaca 1920 gtggctggaa gtctaaacga tttcagctac ctccatacaa actgctttga gctgtccatc 1980 tacgtgggct gtgataaata cccacacgag agcgagctgc cggaggaatg ggagaataac 2040

```
cgggagtete tgattgtgtt catggageag gttcategag gcateaaagg catagtgaga 2100
gatttacaag ggaaagggat ttcaaatgct gtcatctctg tggaaggtgt taaccatgac 2160
atccggacag ccagcgatgg ggattactgg cgtctactga accctggcga atatgtggtc 2220
acagccaagg cggaaggctt tatcacttcc accaagaact gcatggttgg ctatgatatg 2280
ggagetaete ggtgtgaett caeceteaca aagaecaaee tggetaggat aagagaaatt 2340
atggagacat ttgggaagca gcctgtcagc ctaccctcca ggcgcctgaa gctgcgggga 2400
cggaaaaggc ggcagcgtgg gtgaccctgt cggacacttg agacataccc cagaccgtgc 2460
aaataaaaat ccactccagt agtaaaaaa
<210> 2
<211> 764
<212> PRT
<213> Mus musculus
<400> 2
Met Ala Arg Leu Gly Thr Ala Cys Pro Ala Leu Ala Leu Ala Leu Ala
Leu Val Ala Val Ala Leu Ala Gly Val Arg Ala Gln Gly Ala Ala Phe
                                25
Glu Glu Pro Asp Tyr Tyr Ser Gln Glu Leu Trp Arg Arg Gly Arg Tyr
                            40
                                                45
Tyr Gly His Pro Glu Pro Glu Pro Glu Pro Glu Leu Phe Ser Pro Ser
                        55
                                            60
Met His Glu Asp Leu Arg Val Glu Glu Glu Glu Gln Glu Pro His
                   70
                                        75
Gln Gln Gly His Arg Thr Pro Lys Lys Ala Ile Lys Pro Lys Lys Ala
                85
                                    90
Pro Lys Arg Glu Lys Leu Val Ala Glu Thr Pro Pro Pro Gly Lys Asn
           100
                                105
                                                    110
Ser Asn Arg Lys Gly Arg Arg Ser Lys Asn Leu Glu Lys Ala Ala Ser
       115
                            120
                                                125
Asp Asp His Gly Val Pro Val Ala His Glu Asp Val Arg Glu Ser Cys
                        135
Pro Pro Leu Gly Leu Glu Thr Leu Lys Ile Thr Asp Phe Gln Leu His
                                        155
Ala Ser Thr Ser Lys Arg Tyr Gly Leu Gly Ala His Arg Gly Arg Leu
                165
                                    170
Asn Ile Gln Ala Gly Ile Asn Glu Asn Asp Phe Tyr Asp Gly Ala Trp
                                185
Cys Ala Gly Arg Asn Asp Leu His Gln Trp Ile Glu Val Asp Ala Arg
                           200
                                                205
Arg Leu Thr Lys Phe Thr Gly Val Ile Thr Gln Gly Arg Asn Ser Leu
                        215
                                            220
Trp Leu Ser Asp Trp Val Thr Ser Tyr Lys Val Met Val Ser Asn Asp
                   230
                                        235
Ser His Thr Trp Val Thr Val Lys Asn Gly Ser Gly Asp Met Ile Phe
                245
                                    250
Glu Gly Asn Ser Glu Lys Glu Ile Pro Val Leu Asn Glu Leu Pro Val
           260
                                265
Pro Met Val Ala Arg Tyr Ile Arg Ile Asn Pro Gln Ser Trp Phe Asp
       275
                           280
                                                285
Asn Gly Ser Ile Cys Met Arg Met Glu Ile Leu Gly Cys Pro Leu Pro
                        295
Asp Pro Asn Asn Tyr Tyr His Arg Arg Asn Glu Met Thr Thr Asp
                    310
                                        315
Asp Leu Asp Phe Lys His His Asn Tyr Lys Glu Met Arg Gln Leu Met
                325
                                    330
Lys Val Val Asn Glu Met Cys Pro Asn Ile Thr Arg Ile Tyr Asn Ile
                                345
                                                    350
Gly Lys Ser His Gln Gly Leu Lys Leu Tyr Ala Val Glu Ile Ser Asp
```

His Pro Gly Glu His Glu Val Gly Glu Pro Glu Phe His Tyr Ile Ala 375 Gly Ala His Gly Asn Glu Wal Leu Gly Arg Glu Leu Leu Leu Leu Leu 390 395 Leu His Phe Leu Cys Gln Glu Tyr Ser Ala Gln Asn Ala Arg Ile Val 405 410 Arg Leu Val Glu Glu Thr Arg Ile His Ile Leu Pro Ser Leu Asn Pro 425 420 Asp Gly Tyr Glu Lys Ala Tyr Glu Gly Gly Ser Glu Leu Gly Gly Trp 440 435 Ser Leu Gly Arg Trp Thr His Asp Gly Ile Asp Ile Asn Asn Asn Phe 455 460 Pro Asp Leu Asn Ser Leu Leu Trp Glu Ala Glu Asp Gln Gln Asn Ala 470 475 Pro Arg Lys Val Pro Asn His Tyr Ile Ala Ile Pro Glu Trp Phe Leu 490 Ser Glu Asn Ala Thr Val Ala Thr Glu Thr Arg Ala Val Ile Ala Trp 505 Met Glu Lys Ile Pro Phe Val Leu Gly Gly Asn Leu Gln Gly Glu Glu 520 Leu Val Val Ala Tyr Pro Tyr Asp Met Val Arg Ser Leu Trp Lys Thr 535 540 Gln Glu His Thr Pro Thr Pro Asp Asp His Val Phe Arg Trp Leu Ala 550 555 Tyr Ser Tyr Ala Ser Thr His Arg Leu Met Thr Asp Ala Arg Arg Arg 565 570 Val Cys His Thr Glu Asp Phe Gln Lys Glu Glu Gly Thr Val Asn Gly 585 Ala Ser Trp His Thr Val Ala Gly Ser Leu Asn Asp Phe Ser Tyr Leu 600 605 His Thr Asn Cys Phe Glu Leu Ser Ile Tyr Val Gly Cys Asp Lys Tyr 615 620 Pro His Glu Ser Glu Leu Pro Glu Glu Trp Glu Asn Asn Arg Glu Ser 630 635 Leu Ile Val Phe Met Glu Gln Val His Arg Gly Ile Lys Gly Ile Val 645 650 Arg Asp Leu Gln Gly Lys Gly Ile Ser Asn Ala Val Ile Ser Val Glu 665 Gly Val Asn His Asp Ile Arg Thr Ala Ser Asp Gly Asp Tyr Trp Arg 680 Leu Leu Asn Pro Gly Glu Tyr Val Val Thr Ala Lys Ala Glu Gly Phe 695 Ile Thr Ser Thr Lys Asn Cys Met Val Gly Tyr Asp Met Gly Ala Thr 710 715 Arg Cys Asp Phe Thr Leu Thr Lys Thr Asn Leu Ala Arg Ile Arg Glu 725 730 Ile Met Glu Thr Phe Gly Lys Gln Pro Val Ser Leu Pro Ser Arg Arg 740 745 Leu Lys Leu Arg Gly Arg Lys Arg Arg Gln Arg Gly

```
<210> 3
<211> 200
<212> DNA
```

<213> Artificial Sequence

<220>

<223> Targeting Vector

<400> 3

ggcatggccc gtctggggac cgcctgçcct gcgctggcgc tggccctggc acttgtggcg 60 gtggccctgg ctggagtcag agcccagggc gcagccttcg aggagcctga ctattacagc 120 caggagetet ggeggegegg gegetattat gggeateegg ageetgagee ggageeggag 180 ctcttctcgc cttcaatgca <210> 4 <211> 200 <212> DNA <213> Artificial Sequence <220> <223> Targeting Vector <400> 4 gagggagaag ttagttgcag agacgcctcc accaggtaac ttttgcatcg ggcagcccga 60 gggggcgcca gcgatcgtgg cactccaggg gacacctggc ttccagtatg ttttcttgag 120 tgagcccagc caaagtcctg tggtgcctgt gttattccct agagactaca tctgagctaa 180 gttcagcttt ctctccctgc 200